

OIPE

RAW SEQUENCE LISTING

DATE: 07/18/2001

PATENT APPLICATION: US/09/896,791

TIME: 13:15:34

Input Set : A:\00244-WO.txt

Output Set: N:\CRF3\07182001\I896791.raw

4 <110> APPLICANT: Berkenstam
 6 <120> TITLE OF INVENTION: Screening methods
 8 <130> FILE REFERENCE: 00244
 C-10 10 <140> CURRENT APPLICATION NUMBER: US/09/896,791
 C-11 11 <141> CURRENT FILING DATE: 2001-06-29
 13 <160> NUMBER OF SEQ ID NOS: 3
 15 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply
 Corrected Diskette Needed

ERRORED SEQUENCES

17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 460
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Mus musculus
 22 <300> PUBLICATION INFORMATION:
 23 <308> DATABASE ACCESSION NO: GenBank / AA028416
 24 <309> DATABASE ENTRY DATE: 1996-09-16
 26 <400> SEQUENCE: 1
 27 gccatggcgt tggggctgca ggcgctgagg tcgaacaccg agctgcggaa ggagaagtcg 60
 28 cgggaccgcc cgcagccggc gcacgaggag acggaggtgc tgtaccagct ggcgcacact 120
 E--> 29 ctgccctttg cgcgcggcgt cacacdnthc tggacaaggg ctccatcatg cgcctcacaa 180
 E--> 30 tcagctacct gcgcatgacc gcctctgcgc acagattgga aaaaggggga gagccactgg 240
 31 acgcctgcta cctgaaggcc ctggagggtt tcgtcatggt actcaccgcc gagggagaca 300
 32 tggcttacct gtcggaaaat gtcagcaagc acctgggcct cagtcagtgg acctctgttc 360
 33 ctctccctg atacataacc cactcctgg taccaatttc tctctggagc tcattggaca 420
 34 cagtatcttt gattttatca tccctgtgac caagaggaac 460
 134 <210> SEQ ID NO: 3
 135 <211> LENGTH: 307
 136 <212> TYPE: PRT
 137 <213> ORGANISM: Mus musculus
 139 <400> SEQUENCE: 3
 140 Met Ala Leu Gly Leu Gln Arg Val Arg Ser Asn Thr Glu Leu Arg Lys
 141 1 5 10 15
 142 Glu Lys Ser Arg Asp Ala Ala Arg Ser Arg Arg Ser Gln Glu Thr Glu
 143 20 25 30
 144 Val Leu Tyr Gln Leu Ala His Thr Leu Pro Phe Ala Arg Gly Val Ser
 145 35 40 45
 146 Ala His Leu Asp Lys Ala Ser Ile Met Arg Leu Thr Ile Ser Tyr Leu
 147 50 55 60
 148 Arg Met His Arg Leu Cys Ala Ala Gly Gly Lys Arg Gly Arg Ala Thr
 149 65 70 75 80
 150 Gly Arg Leu Leu Pro Glu Gly Pro Gly Gly Phe Arg His Gly Thr His
 151 85 90 95
 152 Arg Arg Gly Arg His Gly Leu Pro Val Gly Lys Cys Gln Gln Ala Pro
 153 100 105 110
 154 Gly Pro Gln Ser Val Asp Leu Cys Ser Ser Ser Leu Ile His Asn Pro

→ see
 item 9 on
 Error
 Summary
 Sheet.

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DATE: 07/18/2001

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Output Set: N:\CRF3\07182001\I896791.raw

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155          115          120          125
156 Thr Pro Gly Thr Asn Phe Ser Leu Glu Leu Ile Gly His Ser Ile Phe
157          130          135          140
158 Asp Phe Ile His Pro Cys Asp Gln Glu Glu Leu Gln Asp Ala Leu Thr
159 145          150          155          160
160 Pro Arg Pro Asn Leu Ser Lys Lys Lys Leu Glu Ala Pro Thr Glu Arg
161          165          170          175
162 His Phe Ser Leu Arg Met Lys Ser Thr Leu Thr Ser Arg Gly Arg Thr
163          180          185          190
164 Leu Asn Leu Lys Ala Ala Thr Trp Lys Val Leu His Cys Ser Gly His
165          195          200          205
166 Met Arg Ala Tyr Lys Pro Pro Ala Gln Thr Ser Pro Ala Gly Ser Pro
167          210          215          220
168 Arg Ser Glu Pro Pro Leu Gln Cys Leu Val Leu Ile Cys Glu Ala Ile
169 225          230          235          240
170 Pro Gln Leu Pro Phe His Asp Gly Ala Thr Leu Gly Leu Pro Gln Glu
171          245          250          255
172 Lys Thr Pro Ile Ser Thr Leu Phe Thr Pro Leu Trp Lys Ala Leu Leu
173          260          265          270
174 Cys Leu Val Lys Arg Trp Pro Val Gln Val Leu Gln Gly Lys Gly Thr
175          275          280          285
176 Glu Ser Ser Leu Pro Ser Trp Val Leu Trp Ala Leu Asn Arg Lys Asn
177          290          295          300
178 Cys Pro Gly
179 305

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E--> 184 00244-WO

E--> 187 - 1 -

delete

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/896,791

DATE: 07/18/2001

TIME: 13:15:35

Input Set : A:\00244-WO.txt

Output Set: N:\CRF3\07182001\I896791.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:29 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
M:340 Repeated in SeqNo=1
L:184 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:187 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

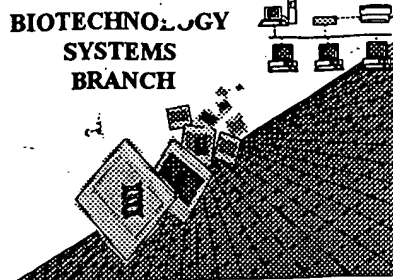
SERIAL NUMBER: 09/896,791

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- Numbering
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- "bug"
- 7 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
 Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
 "bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

RAW SEQUENCE LISTING **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/896,791

Source: OIPK

Date Processed by STIC: 7/18/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>